calling said unknown base according to <u>results of said comparing step</u> [**said comparison of said plurality of probe intensities**].

3.   (Amended) The method of claim <u>1</u> [2], <u>wherein said comparing step includes</u> [**further comprising**] the step of said computer system calculating a ratio of a higher probe intensity to a lower probe intensity.

4.   (Amended) The method of claim 3, <u>wherein said calling step includes</u> [**further comprising**] the step of calling said unknown base as being a base <u>according to</u> [complement of] said probe associated with said higher probe intensity if said ratio is greater than a predetermined ratio value.

6.   (Amended) The method of claim <u>1</u> [2], further comprising the step of sorting said plurality of probe intensities.

8.   (Amended) The method of claim 7, <u>wherein said comparing step includes</u> [**further comprising**] the step of said computer system comparing probe intensities of a probe hybridizing with said sample sequence to probe intensities hybridizing with said reference sequence.

9.   (Amended) The method of claim 7, <u>wherein said comparing step includes</u> [**further comprising**] the step of calculating first ratios of a wild-type probe intensity to each probe intensity of a probe hybridizing with said reference sequence, wherein said wild-type probe intensity is associated with a wild-type probe.

10.   (Amended) The method of claim 9, <u>wherein said comparing step includes</u> [**further comprising**] the step of calculating second ratios of the highest probe intensity of a probe hybridizing with said sample sequence to each probe intensity of a probe hybridizing with said sample sequence.

11. (Amended) The method of claim 10, <u>wherein said comparing step includes</u> [**further comprising**] the step of calculating <u>third</u> ratios of said first ratios to said second ratios.

12. (Amended) The method of claim <u>46</u> [7], <u>wherein said comparing step includes</u> [**further comprising**] the step of comparing <u>said ratio of neighboring nucleic acid probes</u> [**neighboring probe intensities of said plurality of probe intensities**].

14. (Amended) The method of claim 13, <u>wherein said comparing step includes</u> [**further comprising**] the step of said computer system comparing probe intensities of a probe hybridizing with said sample sequence to statistics about said plurality of experiments.

Please add claims 45-59 as follows.

-- 45. The method of claim 11, wherein said calling step includes the step of calling said unknown base according to said probe associated with a highest third ratio.

46. The method of claim 7, wherein said comparing step includes the step of calculating a ratio of a highest probe intensity of a probe hybridizing with said reference sequence to a highest intensity of a probe hybridizing with said sample sequence.

47. In a computer system, a method of identifying an unknown base in a sample nucleic acid sequence, said method comprising the steps of:
    inputting a plurality of probe intensities, each of said probe intensities being associated with a nucleic acid probe;
    said computer system comparing said plurality of probe intensities wherein each of said plurality of probe intensities

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is substantially proportional to said associated nucleic acid
probe hybridizing with said sample sequence; and

    calling said unknown base according to results of said
comparing step.

    48. The method of claim 47, wherein said comparing
step includes the step of said computer system calculating a
ratio of a higher probe intensity to a lower probe intensity.

    49. The method of claim 48, wherein said calling step
includes the step of calling said unknown base according to said
probe associated with said higher probe intensity if said ratio
is greater than a predetermined ratio value.

    50. The method of claim 49, wherein said predetermined
ratio value is approximately 1.2.

    51. In a computer system, a method of identifying an
unknown base in a sample nucleic acid sequence, said method
comprising the steps of:

    inputting a first set of probe intensities, each of
said probe intensities in said first set being associated with a
nucleic acid probe and substantially proportional to said
associated nucleic acid probe hybridizing with a reference
nucleic acid sequence;

    inputting a second set of probe intensities, each of
said probe intensities in said second set being associated with a
nucleic acid probe and substantially proportional to said
associated nucleic acid probe hybridizing with said sample
sequence;

    said computer system comparing at least one of said
probe intensities in said first set and at least one of said
probe intensities in said second set; and

    calling said unknown base according to results of said
comparing step.

52. The method of claim 51, wherein said comparing
step includes the steps of:

calculating first ratios of a wild-type probe intensity
to each probe intensity of a probe hybridizing with said
reference sequence, wherein said wild-type probe intensity is
associated with a wild-type probe; and

calculating second ratios of the highest probe
intensity of a probe hybridizing with said sample sequence to
each probe intensity of a probe hybridizing with said sample
sequence.

53. The method of claim 52, wherein said comparing
step further includes the step of calculating third ratios of
said first ratios to said second ratios.

54. The method of claim 53, wherein said calling step
includes the step of calling said unknown base according to said
probe associated with a highest third ratio.

55. The method of claim 51, wherein said comparing
step includes the step of calculating a ratio of a highest probe
intensity in said first set to a highest intensity in said second
set.

56. The method of claim 55, wherein said comparing
step further includes the step of comparing said ratio of
neighboring nucleic acid probes.

57. In a computer system, a method of identifying an
unknown base in a sample nucleic acid sequence, said method
comprising the steps of:

inputting statistics about a plurality of experiments,
each of said experiments producing probe intensities each being
associated with a nucleic acid probe and substantially
proportional to said associated nucleic acid probe hybridizing
with a reference nucleic acid sequence;